

Two-site evaluation of the relationship between *in vivo* and carcass dual energy X-ray absorptiometry (DXA) in pigs

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Received 27 March 2006; received in revised form 27 March 2006; accepted 29 May 2006

Abstract

A study was conducted to compare swine body composition measurements (fat tissue, lean tissue and bone mineral) made by DXA *in vivo* and on the right carcass half using two GE Lunar DPX pencil beam instruments at two different locations. Pigs weighing between 60 and 105 kg were first scanned *in vivo* by DXA and after slaughter the right carcass half of each pig was scanned — 78 pigs at the USDA in Beltsville, MD using a GE Lunar DPX-L instrument and 62 pigs at the LVG in Oberschleissheim, Germany using a GE Lunar DPX-IQ instrument (an updated model of the DPX-L). In addition to a separate analysis, despite confounding effects likely caused by the different study locations and probe preparations (scan modes) the data were pooled. Based on linear regression analysis of the pooled data, the relationship between DXA carcass half (dependent variable) and *in vivo* measurements resulted in coefficients of determination (R^2) of 0.58 for fat percentage ($\sqrt{\text{MSE}}=3.82\%$) and of 0.52 for lean percentage ($\sqrt{\text{MSE}}=4.09\%$). The R^2 values were expectedly higher when the data sets were analyzed separately for each location: 0.79 ($\sqrt{\text{MSE}}=2.38\%$) and 0.85 ($\sqrt{\text{MSE}}=1.60\%$) for fat percentage and 0.79 ($\sqrt{\text{MSE}}=2.41\%$) and 0.84 ($\sqrt{\text{MSE}}=1.65\%$) for lean percentage at USDA and LVG, respectively. Regardless of the relatively close relationship among *in vivo* and carcass results for the pooled data, caution is advised in comparing measurements among GE Lunar DPX-L and DPX-IQ instruments, since the residuals ($\sqrt{\text{MSE}}$) for the regression analysis of DXA FAT% and DXA LEAN% measurements exceed 2.5%. © 2006 Elsevier B.V. All rights reserved.

Keywords: Dual energy X-ray absorptiometry; Body composition; *In vivo*; Carcass

1. Introduction

Dual energy X-ray absorptiometry is becoming a more frequently used technology in farm animal research in order to study for example the *in vivo* changes in the body composition of pigs (Mitchell et al., 1996; Mitchell

and Pursel, 2003; Suster et al., 2003), the carcass composition of sheep (Knott et al., 2003), or pigs (Mitchell et al., 1998; Marcoux et al., 2001; Scholz et al., 2002), the *in vivo* body composition of broilers (Buyse et al., 2003) or calves (Scholz et al., 2003; Hampe et al., 2005). A goal of live animal measurements is to predict carcass traits that are determinants of carcass value. However so far, there is limited data available regarding the relationship between *in vivo* DXA and carcass DXA data for the body composition of pigs — the main focus of the present study. A study by Suster et al. (2003), using a Hologic DXA, reported similar precision for

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Table 1
Set up for both experiments

Location	Growth Biology Laboratory of the USDA, Beltsville (USDA)	Experimental Farm Oberschleissheim, Ludwig-Maximilians University Munich (LVG)
DXA scanner	GE Lunar DPX-L	GE Lunar DPX-IQ
Body weight (kg)	60–105	
Age (days)	88–238	
Whole body software mode(s)	Adult slow (0.03 mrem), Adult medium (0.02 mrem)	Adult “normal” (0.03 mrem)
Pixel size	4.8 × 9.6 mm	
Software version	4.6d	4.7e
Number of animals	77	62
Sex of animals	Males, male castrates, females	Male castrates, females
Genetic origin of animals	US Landrace (LR), Poland China × LR, different synthetic lines (with varying proportions of Duroc, Hampshire, Poland China, Spotted, Yorkshire)	Pietrain (Pi), Pi × different sow lines
Days between <i>in vivo</i> and carcass scan (slaughtering)	3	
Carcass DXA analysis	Without head (eviscerated carcass halves)	
Carcass weight (kg)	21–38	
Carcass software mode(s)	Adult medium	Adult “normal”

whole body, whole carcass and half-carcass scans at predicting chemical measurements of the masses of carcass lean, water, protein, fat and ash within and across experiments using pigs from 10 to 120 kg live weight. Additionally, there is a large variation in body composition measurements among manufacturers of DXA scanners (Kistorp and Svendsen, 1997; Tothill and Hannan, 2000, 2002), while the variation of results for comparable devices (e.g. pencil and/or fan beam scanners) of a single manufacturer is supposed to be very small (Tataranni et al., 1996; Oldroyd et al., 1998, 2003). One manufacturer (GE Lunar) provides for its series of DXA scanners formulas for the transformation

of results of other manufacturers (Hologic, Norland) but no formulas within the own series of DXA scanners.

The purpose of the present experiment was to evaluate two different models of DXA scanners at two different locations for measuring the composition of the live pig and carcass and to examine the relationship between the live and carcass measurements at both locations.

Though different probes were used, this two-site study additionally attempts to validate, whether the body composition measurements for pencil beam DXA scanners of the same manufacturer (GE Lunar DPX-L and DPX-IQ) are comparable.

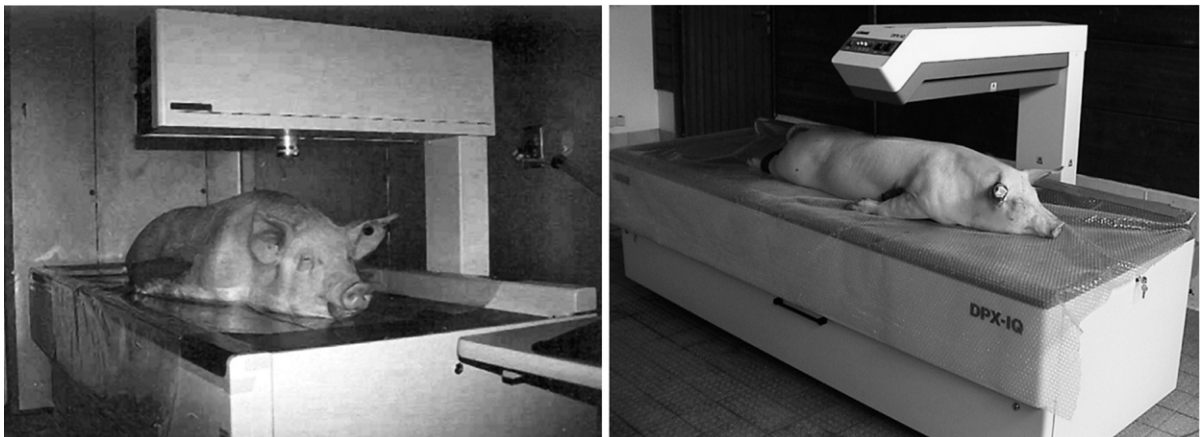


Fig. 1. *In vivo* positioning of the pigs on the GE Lunar DPX-L (left) and on the GE Lunar DPX-IQ (right) for a whole body analysis.

2. Materials and methods

2.1. Animals and experimental sites

Two experiments¹ were performed at two different locations as summarized in Table 1. The first DXA scan was performed *in vivo* under sedation (Fig. 1). Subsequently (three days after the scan *in vivo*), the right carcass half (always without viscera: including all internal organs, associated fat, and leaf fat) was scanned as DXA reference side (Fig. 2). At both locations after slaughter, the carcasses were split at the midline. The tail had been docked, but remained on the carcass without regard to right or left. Hair, feet and skin remained on the carcasses.

The head (including jawl) was removed at the 1st cervical vertebrae at the USDA, while the head (one half) remained on the carcass half at the LVG, but was not included in the analysis. The differences in the positioning of the carcasses on the DXA tables (Fig. 2) did not affect the DXA readings, since it does not matter whether the carcass half lies on the skin or on the other side (see Lukaski et al., 1999).

The body composition measurements with the total-body GE Lunar DXA scanners (DPX-L, DPX-IQ) are based on the relative tissue (bone, fat, lean) absorbance of X-radiation at two energy levels (k-edge filter low: 38 keV; high: 70 keV) by using a constant X-ray source of 76 kVp and assuming a fixed water content of 73–74% within the lean tissue (Roubenoff et al., 1993; Laskey, 1996; Pietrobelli et al., 1998).

The maximum scan area measures 619 mm × 1958 mm, equivalent to 204 scan lines, each line consisting of a maximum of 128 pixels with a sample or pixel size of 4.8 × 9.6 mm at the velocities used for both scanners within the whole body adult mode. Two scan settings were used with the DPX-L scanner with the following “velocities” and durations (maximum time for a complete scan): “medium” (19 min), “slow” (37 min). For the DPX-IQ scanner the “normal” (28 min) mode (and the “schnell” mode, 14 min, for the variable composition phantom) was applied.

Each pixel is analyzed as consisting of two compartments. In pixels with soft tissue only (X-ray attenuation coefficient = R value ≤ 1.455 ; theoretical R for $H_2O = 1.3572$), the scanning software distinguishes between fat (theoretical $R = 1.2058$ – 1.2333) and non-fat (lean) tissue

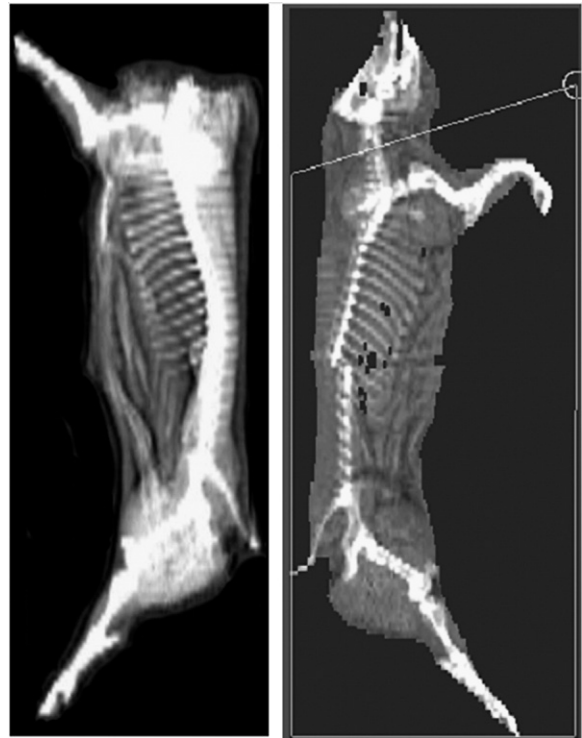


Fig. 2. Right carcass half positioning (with regions of interest for data analysis); left: USDA, right: LVG.

($1.2333 < R < 1.455$). In the presence of bone (very high R value; ≥ 2.8617), it distinguishes between bone and soft tissue (Pietrobelli et al., 1996, 1998; Testolin et al., 2000).

After the scans *in vivo*, data were analyzed as standard (automatic) analysis at LVG. The USDA *in vivo* scans were analyzed using the “extended research analysis” option. For the half carcasses, data were analyzed as extended (manual) analysis, where a special filtration technique is used within the manually defined regions of interest. As long as the defined regions of interest cover the whole area of the scanned object (pig), there is no difference between the results of the standard and extended analysis — at least for the software version 4.7e.

2.2. Housing/feeding

At the USDA, between a body weight of approximately 30 kg and the final body weight (<105 kg), the pigs were individually housed on partly slatted concrete floor and fed at 95–100% of estimated voluntary intake (NRC, 1988) a diet containing 17.62% protein and an ME content of 14.12 MJ/kg. At LVG also starting at

¹ These studies were conducted in accordance with protocols approved by the Government of Upper Bavaria with the tracking numbers 211-2531.2-21/2000; 209.1/211-2531-46/02 and by the USDA-ARS, Beltsville Animal Care and Use committee.

Table 2

Means, standard deviations and t-test results of DXA variables comparing the two sites

Variable*	Unit	LVG (<i>n</i> =62)		USDA (<i>n</i> =77)		Difference <i>P</i> value
		Mean	Std dev	Mean	Std dev	
	<i>In vivo</i>					
R_K		1.351	0.010	1.348	0.011	0.044
FATPCK	%	19.53	4.84	20.28	5.17	0.38
FATK	g	15,843	5364	17,697	5801	0.053
LEANPCK	%	77.66	5.01	77.42	5.15	0.78
LEANK	g	61,603	6787	66,159	8184	<0.001
BMCK	g	2258	480	1964	292	<0.001
BMPCCK	%	2.81	0.27	2.30	0.22	<0.001
DXWTK	g	79,704	10,477	85,819	11,603	0.002
	Carcass half (without head)					
R_H		1.368	0.009	1.352	0.011	<0.001
FATPCH	%	11.55	4.06	18.61	5.21	<0.001
FATH	g	3281	1522	5932	2082	<0.001
LEANPCH	%	85.98	4.07	78.80	5.18	<0.001
LEANH	g	23,573	3195	24,603	3214	0.062
BMCH	g	682	142	813	140	<0.001
BMPCH	%	2.47	0.25	2.59	0.23	0.003
DXWTH	g	27,537	4336	31,347	4425	<0.001

*R=soft tissue X-ray attenuation coefficient; K=*in vivo* data; H=half-carcass data; FATPC=Fat Percentage; LEANPC=Lean Percentage; BMC=Bone Mineral Content; BMPC=Bone Mineral Percentage; DXWT=DXA Weight.

30 kg, the pigs were kept in groups of 20–22 pigs on fully slatted floors, but were fed at 75–80% of estimated voluntary feed intake (NRC, 1988) a diet containing 17.7% protein and 14.0 MJ/kg of ME to a body weight of 75 kg; thereafter the diet contained 16.2% protein and 13.7 MJ/kg of ME.

2.3. Variable Composition Phantom (VCP)

In order to study the effect of different scan velocities (adult “normal” vs. adult “schnell”) under standardized conditions, a Variable Composition Phantom (VCP) of Bio-Imaging Technologies, Inc., Newton, PA, was used on the DPX-IQ at LVG. The VCP is a DXA phantom for

calibration of soft tissue body composition. It consists of 4 rectangular acrylic blocks [each $20.3 \times 24.8 \times 13.3$ cm], with an aluminium “head” to simulate the skull (bone mineral). Four different vinyl sheets are used in different combinations to simulate low (8%), medium (25%) and high (45%) fat content.

The VCP was scanned on both scan modes 4 times with each fat set up.

2.4. Data analysis and statistics

The effects of genotype and sex were not included in this site comparison. According to a preliminary subpopulation regression analysis (data not shown) comparing the

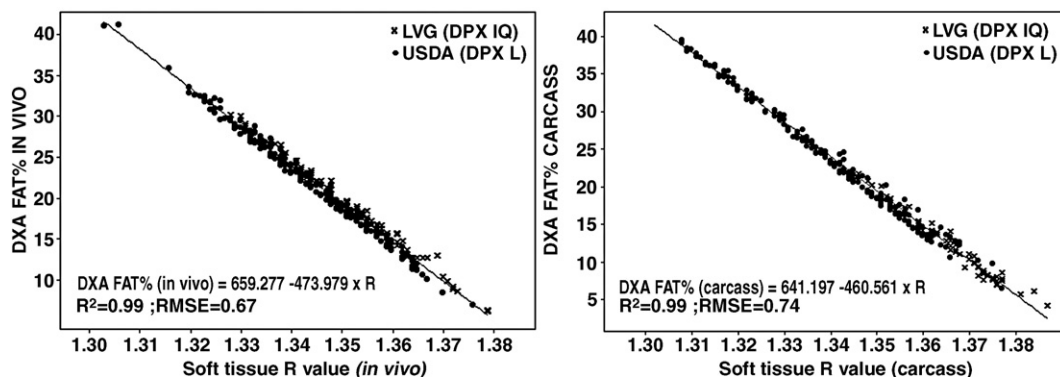


Fig. 3. Relationship between the DXA soft tissue X-ray attenuation coefficient (R_{st} value) and the DXA fat percentage (Fat %) for the combined sets of the *in vivo* (left) and carcass (right) data.

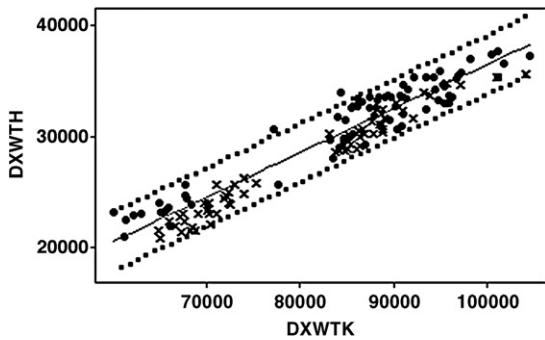


Fig. 4. Relationship between the DXA tissue weights (DXWT, g) for the pooled sets of the *in vivo* (K) and carcass half (H) data (dotted lines mark the 95% confidence interval of prediction); dots=USDA data; crosses=LVG data.

separate intercepts and slopes for male and female pigs of the variable studied (using a *t* test), sex did not affect significantly the relationship between *in vivo* and carcass data. In addition within each location, genotype did not affect significantly the relationship between *in vivo* and carcass data. But, genotype and/or sex differences between both sites could affect (bias) the relationship within the pooled data set. However, neither genotype nor sex effect could be separated from the site effect due the use of different genotypes and sexes at both sites (Table 1).

Measurements between the two sites (swine study, Table 2) and the two scan velocities (VCP study) were compared using a two-sided *t*-test (proc *t*-test; SAS 8.2, Cary, NY). The level of significance – after approving equal or unequal variances with the *F* test performed – was chosen at $P < 0.05$.

A linear regression analysis using the “proc reg” module of the SAS statistics package 8.2 was performed to calculate the relationship between *in vivo* and carcass

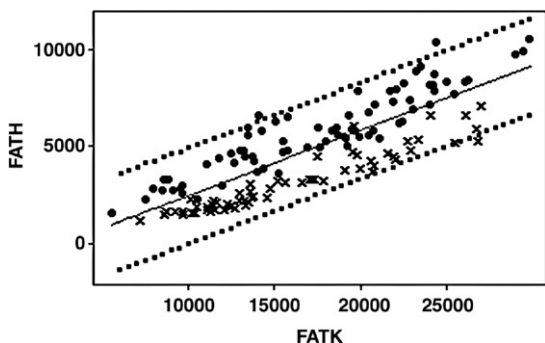


Fig. 5. Relationship between the DXA fat tissue weights (FAT, g) for the pooled sets of the *in vivo* (K) and carcass half (H) data (dotted lines mark the 95% confidence interval of prediction); dots=USDA data; crosses=LVG data.

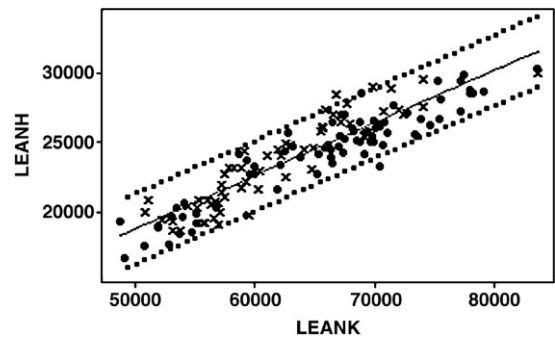


Fig. 6. Relationship between the DXA lean tissue weights (LEAN, g) for the pooled sets of the *in vivo* (K) and carcass half (H) data (dotted lines mark the 95% confidence interval of prediction); dots=USDA data; crosses=LVG data.

data for the pooled data sets and separately for both sites. The traits of the carcass half were used as dependent variable in the regression analysis.

The coefficients of determination (R^2) and the root mean square errors (RMSE or $\sqrt{\text{MSE}}$, and synonymously standard error of estimation — SEE) were calculated for the different data sets:

$$\text{SEE} = \text{RMSE} = \sqrt{\text{MSE}} = \sqrt{s_y^2 - R_{Y/X} \cdot s_{xy}} = \sqrt{s_y^2 - \frac{s_{xy}^2}{s_x^2}} = s_y \sqrt{1 - r^2}.$$

3. Results

3.1. *In vivo* vs. carcass

As expected, there existed a very high relationship between the whole body DXA soft tissue X-ray attenuation coefficient (*R*) and the DXA fat percentage (DXA Fat %) for the pooled sets of the *in vivo* and

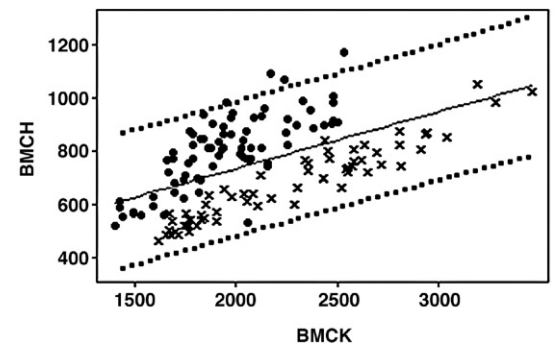


Fig. 7. Relationship between the DXA bone mineral (BM, g) for the pooled sets of the *in vivo* (K) and carcass half (H) data (dotted lines mark the 95% confidence interval of prediction); dots=USDA data; crosses=LVG data.

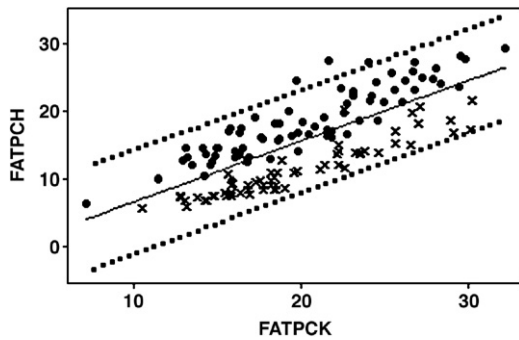


Fig. 8. Relationship between the DXA fat proportion (FAT, %) for the pooled sets of the *in vivo* (K) and carcass half (H) data (dotted lines mark the 95% confidence interval of prediction); dots=USDA data; crosses=LVG data.

carcass data (Fig. 3), consistent with the same technical and software basis for both DXA scanners.

In addition, the relationship between *in vivo* and carcass DXA data attained a medium to high level for the pooled data if the tissue masses (DXA Weight, g; DXA Lean, g; DXA Fat, g; DXA Bone Mineral, g) were compared (Figs. 4–7). The agreement was lower for the corresponding percentage values of DXA fat, lean, and bone mineral (Figs. 8–10). Compared to the USDA results, the LVG carcass measurements had lower DXA Fat % and higher DXA Lean % relative to the measurements *in vivo*. Based on the data shown in Table 2, comparing the live measurements to the carcass measurements (carcass half $\times 2$), the DXA weight difference was 24,360 g (30% of live weight) for LVG and 23,124 g (27%) for USDA. The difference in lean tissue mass was 14,457 g (23%) for LVG and 16,953 g (25%) for USDA. There were greater discrepancies between LVG and USDA measurements for fat and BMC. The difference in fat tissue mass was 9281 g

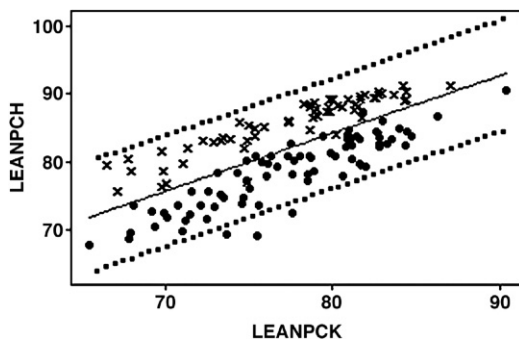


Fig. 9. Relationship between the DXA lean proportion (Lean, %) for the pooled sets of the *in vivo* (K) and carcass half (H) data (dotted lines mark the 95% confidence interval of prediction); dots=USDA data; crosses=LVG data.

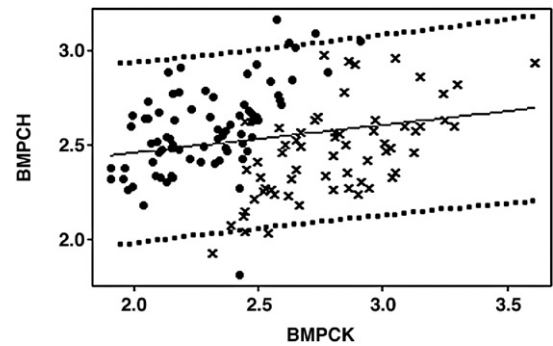


Fig. 10. Relationship between the DXA bone mineral proportion (BMPC) for the pooled sets of the *in vivo* (K) and carcass half (H) data (dotted lines mark the 95% confidence interval of prediction); dots=USDA data; crosses=LVG data.

(59%) for LVG and 5833 g (33%) for USDA. The difference in BMC was 893 g (39%) for LVG and 337 g (17%) for USDA.

The smallest agreement between *in vivo* and carcass DXA data existed for the bone mineral percentage (pooled data: DXA Bone Mineral %: $R^2=0.04$, $\sqrt{\text{MSE}}=0.24$; $\text{BMPCH}=2.167 [0.147 \text{ standard error}] + 0.147 [0.058 \text{ standard error}] \text{ BMPCK}$), while the *in vivo* and carcass DXA data agreed very well for the bone mineral density (BMD, g/cm^2 ; only LVG data; Fig. 11). Nonetheless, the absolute BMD level measured *in vivo* was higher ($\bar{X}=1.002$, $s=0.072$; g/cm^2) than that measured in the carcasses ($\bar{X}=0.803$, $s=0.063$; g/cm^2). This observation is in agreement with a positive correlation between soft tissue mass and BMD (g/cm^2) with $r=0.85$ (*in vivo*: adjusted $R^2=0.72$, $\sqrt{\text{MSE}}=0.038$; carcass: adjusted $R^2=0.73$, $\sqrt{\text{MSE}}=0.033$).

Analyzing the two separate data sets led to higher relationships (R^2) between the carcass and *in vivo* DXA data (Table 3) compared to the pooled data set. With exception of the bone mineral measurements (g, and especially %), the carcass data explain within both sites

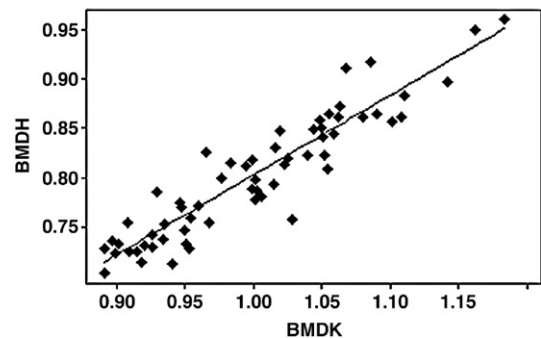


Fig. 11. Relationship between *in vivo* and carcass DXA bone mineral density (BMD, g/cm^2).

Table 3

Adjusted coefficients of variation (R^2), root mean square errors ($\sqrt{\text{MSE}}$), intercepts (a ; in brackets standard error), and slopes (b ; in brackets standard error) for the regression equations of carcass (dependent variable) and *in vivo* DXA data separately for both sites

	USDA	LVG
<i>R</i> soft tiss.	$R^2=0.80$, $\sqrt{\text{MSE}}=0.005$ $a=0.066$ (0.074); $P<0.38$ $b=0.954$ (0.055); $P<0.0001$	$R^2=0.85$, $\sqrt{\text{MSE}}=0.003$ $a=0.320$ (0.056); $P<0.0001$ $b=0.776$ (0.042); $P<0.0001$
Weight (g)	$R^2=0.91$, $\sqrt{\text{MSE}}=1317$ $a=83$ (1127); $P<0.94$ $b=0.364$ (0.013); $P<0.0001$	$R^2=0.97$, $\sqrt{\text{MSE}}=781$ $a=-4921$ (767); $P<0.0001$ $b=0.407$ (0.01); $P<0.0001$
Fat (%)	$R^2=0.79$, $\sqrt{\text{MSE}}=2.38$ $a=0.399$ (1.105); $P<0.72$ $b=0.898$ (0.053); $P<0.0001$	$R^2=0.85$, $\sqrt{\text{MSE}}=1.60$ $a=-3.516$ (0.851); $P=0.0001$ $b=0.771$ (0.042); $P<0.0001$
Fat (g)	$R^2=0.84$, $\sqrt{\text{MSE}}=822$ $a=89.7$ (303); $P<0.77$ $b=0.330$ (0.016); $P<0.0001$	$R^2=0.90$, $\sqrt{\text{MSE}}=471$ $a=-996.2$ (188); $P=0.0001$ $b=0.027$ (0.011); $P<0.0001$
Lean (%)	$R^2=0.78$, $\sqrt{\text{MSE}}=2.41$ $a=9.65$ (4.16); $P<0.023$ $b=0.893$ (0.054); $P<0.0001$	$R^2=0.84$, $\sqrt{\text{MSE}}=1.65$ $a=28.25$ (3.28); $P<0.0001$ $b=0.743$ (0.042); $P<0.0001$
Lean (g)	$R^2=0.87$, $\sqrt{\text{MSE}}=1154$ $a=331$ (1079); $P<0.76$ $b=0.367$ (0.016); $P<0.0001$	$R^2=0.85$, $\sqrt{\text{MSE}}=1257$ $a=-3127$ (1469); $P<0.037$ $b=0.433$ (0.024); $P<0.0001$
BM (%)	$R^2=0.30$; $\sqrt{\text{MSE}}=0.20$ $a=1.268$ (0.231); $P<0.0001$ $b=0.577$ (0.100); $P<0.0001$	$R^2=0.37$; $\sqrt{\text{MSE}}=0.19$ $a=0.919$ (0.257); $P=0.0007$ $b=0.552$ (0.091); $P<0.0001$
BMC (g)	$R^2=0.59$; $\sqrt{\text{MSE}}=90$ $a=91.28$ (70); $P<0.20$ $b=0.367$ (0.035); $P<0.0001$	$R^2=0.90$; $\sqrt{\text{MSE}}=45$ $a=47.25$ (27.5); $P=0.091$ $b=0.281$ (0.012); $P<0.0001$

more than 78% of the variation of the *in vivo* data (adjusted $R^2>0.78$ USDA; $R^2>0.83$ LVG data). Unexpectedly, for each regression equation – with exception of DXA Lean (g) – the LVG data gave a higher R^2 and a lower $\sqrt{\text{MSE}}$. However, with exception of bone mineral, the intercept value (a) for LVG equations were significantly different from zero, but not for the USDA equations.

3.2. Scan velocities (*schnell* vs. *normal* — correspondingly to *medium* vs. *slow*)

A separate study using a Variable Composition Phantom (VCP) from Bio-Imaging Technologies (Newtown, PA) on the DPX IQ (LVG) shows small differences between the two scan modes “*schnell*” and “*normal*” with the “*schnell*” mode resulting in slightly lower R values and correspondingly slightly higher DXA Fat % than the “*normal*” mode. The absolute difference was *highest* ($P=0.003$) at the low fat level with 8.63% reference fat ($\text{SD}=0.45$) for the “*normal*” mode and 10.53% reference fat ($\text{SD}=0.67$) for the “*schnell*” mode (R values 1.300 vs. 1.299) and lowest ($P=0.20$) at the high fat level with 46.08% reference fat ($\text{SD}=0.741$) for the “*normal*” mode and 46.68%

reference fat ($\text{SD}=0.05$) for the “*schnell*” mode (R values 1.375 vs. 1.371). The difference for the medium fat level was also significant ($P=0.039$) with 23.4% reference fat ($\text{SD}=0.356$) for the “*normal*” mode and 24.43% reference fat ($\text{SD}=0.695$) for the “*schnell*” mode (R values 1.345 vs. 1.343).

4. Discussion

Generally, there is little information available about the relationship between corresponding *in vivo* (live) and carcass body composition measurements. The site differences observed for the relationship between *in vivo* and carcass results may depend on various reasons, including instrument/scan mode, pig population (sex, genotype), probe preparations, feeding and housing conditions, or differences in tissue hydration and fat distribution within the body.

A potential bias exists in the pooled data because the data were drawn from two different studies and different populations using two slightly different scan modes (velocities) for the half-carcass scans at both study locations.

However, the scan mode does not affect the relationship between the soft tissue R value and the DXA

calculated fat percentage as indicated by the results shown in Fig. 3 where the USDA DPX-L *in vivo* measurements were made using both the slow and medium scan modes and carcass measurements were made using only the medium mode. In contrary, the scan mode (slow vs. medium or “normal” vs. “schnell”) may slightly influence the reported *R* value (DXA Fat %), which most likely accounts for some of the differences between the USDA and LVG results especially for the half-carcass analysis (Table 1). The combination of less tissue depth and slower scan mode may have resulted in a bias in tissue attenuation.

Though the relative (*in vivo* vs. carcass) lean tissue mass (38.3% and 37.2%) and total tissue mass (34.6% and 36.5%) measurements for LVG and USDA, respectively, are in close agreement. The proportion of “total” BMC measured in the carcass was again lower at LVG (30.2% vs. 41.4%). Additionally, relative to the scan *in vivo* the carcass measured fat percentage was 59.1% at LVG compared to 91.8% at USDA (Table 2). The difference in the total amount of fat measured in the live pig versus its carcass should be accounted for by the amounts of fat removed with the head, the perirenal or leaf fat, and fat associated with the internal organs. Assuming the perirenal (perinephric) fat to be 6% of total body fat (Walstra, 1980; Karégé, 1991, cited by Lizardo et al., 2000), this would – in the average – amount to 950 g for the LVG pigs and 1061 g for the USDA pigs. Assuming the fat content in the head region to be 28% *in vivo* (estimate from USDA and LVG scan data), this would amount to 1500 g for the LVG pigs and 1600 g for the USDA pigs. Considering the 9281 g difference for the LVG live versus carcass fat and 5833 g difference for the USDA live versus carcass, this leaves 6831 g and 3172 g of fat, respectively that was associated with the internal organs or otherwise unaccounted for. With regard to BMC, the total amount of BMC in the head should amount an average approximately 300–350 g. Thus, the 337 g difference for the USDA pigs can be accounted for by head BMC, however the 893 g difference for the LVG pigs leave approximately 550 g unaccounted for. Apparently, a larger amount of carcass tissue is classified as soft lean tissue instead of fat tissue or bone mineral at the DPX-IQ (LVG) when using the adult “normal” mode compared to a mode with higher scan velocity.

Black et al. (2002) found also significant differences among scan modes using a GE LUNAR DPX-IQ. Scanned lean body mass significantly decreased with higher scan velocity and lean body mass was 2.7% lower in “fast” than in “medium” mode ($P < 0.0001$). In contrast, fat mass, percentage of body fat, and bone

mineral contents were higher with increasing scan velocity. Similarly, the present study using a Variable Composition Phantom (VCP) from Bio-Imaging Technologies (Newtown, PA) on the DPX IQ (LVG) shows small differences between the two scan modes “schnell” (fast) and “normal” with the “schnell” mode resulting in slightly lower *R* values and correspondingly slightly higher DXA Fat % than the “normal” mode as shown in the results (Section 3.2).

In addition to the age of the X-ray source (Nord, 1998), slightly different scanner calibrations and/or software versions for the GE Lunar DPX scanner series might explain other differences in relationships between the DPX-L and the DPX-IQ *in vivo* and carcass results. Vozarova et al. (2001) found no significant differences between Lunar Software versions 1.33 and 1.35 on a Lunar DPX-L scanner, while the scan mode affected the DXA Fat % result for the lean tissue phantom used, thus confirming the present VCP results. In contrast, another study by Lantz et al. (1999) found a rather large discrepancy ($P < 0.001$) between two (identical) Lunar DPX-L scanners for body composition measurements on eight individuals with average body fat masses of 13.2 vs. 9.7 kg and lean tissue masses of 47.1 vs. 50.9 kg. The large difference was explained by hardware problems. Diessel et al. (2000) also used a Variable Composition Phantom (VCP) with a given nominal soft tissue composition in order to compare the DXA readings of the GE Lunar pencil beam scanners DPX-IQ (matches LVG), DPX-L (matches USDA) and one EXPERT fan beam scanner. In agreement with the half-carcass results of the USDA-versus-LVG study, the DPX-L scanner gave higher DXA Fat (%) readings than the DPX-IQ scanner with absolute differences between 2.4 and 3.4% DXA Fat.

The direct use of regression equations developed on a DPX-L for the results of a DPX-IQ seems therefore questionable. However based on the VCP data only (Diessel et al., 2000), they might give reasonable results if a linear correction of $Y = 1.0169X - 3.5157$ is used for the transformation of the DPX-L DXA Fat % to the DPX-IQ DXA Fat % results and of $Y = 0.9825X + 3.4806$ for *vice versa*. According to Diessel et al. (2000) it would be incorrect to make corrections or comparisons based on the VCP data alone (or carcass DXA data), since they found a different pattern when including *in vivo* data in the cross-comparison of different DXA scanners like the Hologic QDR-4500 and the GE Lunar DPX IQ. On the other hand, a study by Suster et al. (2003) using a Hologic DXA instrument (whole body scan mode) reported similar precision for *in vivo* and carcass scans relative to reference data.

Expectedly, the relationships for percentage values resulted in lower R^2 values (and higher $\sqrt{\text{MSE}}$) than those based on tissue masses. Furthermore, the low R^2 observed for the relationship between *in vivo* and carcass DXA bone mineral percentage is also due to the small variation in the true percentage of bone mineral either *in vivo* or in the carcass.

It appears also possible, that the different genetic material used in the two studies (see Table 1) might be related to a different distribution of fat and lean tissue within the body as described by Ball (2000), Kolstad et al. (1996), Kolstad (2001a,b), and de Lange et al. (2003) based partly on data of Edwards et al. (2003). A higher proportion of internal fat might lead to a relatively higher DXA fat % *in vivo* but to a relatively low DXA fat % in the carcass half, since the internal fat was not included in the carcass DXA analysis. Another source of error might be the low tissue depth of some areas of the carcass halves (especially side parts) scanned. Laskey and Prentice (1999) found most imprecise results for DXA fat tissue measurements at low tissue depths (<6.8 cm), when the coefficient of variation exceeded 20%.

The different relationships between *in vivo* and carcass DXA results comparing both sites might also depend on the different tissue hydration in growing subjects as was confirmed for children by Testolin et al. (2000) and Wong et al. (2002). The stability of the lean soft tissue R value depends – at least partly – on the constancy of its constituent water ($R=1.3572$), protein ($R=1.2096$), glycogen ($R=1.3010$), and soft tissue mineral ($R \sim 2.8617$) proportions, while the stability of the fat soft tissue R value (1.2058–1.2333) depends on the constancy of its constituent water and lipid (fatty acids and triglycerides) proportions. Any change in these proportions, which is the case in growing animals, under different feeding conditions, and in different (pig) genotypes, would lead to an actual change in the lean or fat soft tissue R value and finally causing errors in DXA fat estimation. The leaner pigs are at the same age or weight, the lower is the lipid content (%) for example in the back fat tissue (Ender et al., 1997; Maignel et al., 1998; Schinckel et al., 2001) or the higher the water content in the back fat tissue with for example 10% in Large Black vs. 23% in Pietrain (Warriss et al., 1990).

Alteration of hydration of the lean tissue would affect the relationship between the DXA measured lean mass and the assumed protein and water content of the lean tissue. Little variation in hydration of the carcass lean tissue would be expected in healthy animals slaughtered at the same stage of maturity. However, *in vivo*, the DXA measurements are more likely to be made at different stages of maturity and the measured lean tissue

includes internal organs and gut fill. Variation in the hydration of the fat tissue as discussed above should not affect the relationship between the DXA measured carcass fat tissue and the *in vivo* one. Results by Testolin et al. (2000) showed a constant relationship between the DXA R value and the percentages of a Ringer lactate–corn oil mixture. Thus, both measurements partition between lipid and water.

Since the DXA experiment at the LVG is mainly based on pure Pietrain or crossbred pigs with 50% Pietrain containing the highest water content in the back fat (Warriss et al., 1990), it seems likely that the DXA carcass fat (%) was underestimated at the LVG relative to the USDA with pigs containing no or less Pietrain, though the water content in the back fat should be the same *in vivo* and in the carcass half. However, because the subcutaneous fat is the main fat component of the carcasses, this DXA fat estimation error (underestimation) would increase in leaner animals explaining at least partly the discrepancies of the relationship between *in vivo* and carcass DXA between both sites. A separate analysis/calibration of DXA data for different pig genotypes with varying water proportions within the fat or lean tissue seems necessary.

Despite the moderate to high general agreement between *in vivo* and carcass results in the pooled data, site-specific constraints have to be considered in multi-site studies using comparable DXA scanners. The results of the pooled data indicate that although there is a close correlation among *in vivo* and carcass DXA for lean and fat tissue (%) measurements with $r \geq 0.72$, caution is advised in comparing measurements among GE Lunar DPX-L and DPX-IQ instruments since the residuals ($\sqrt{\text{MSE}}$) for the regression analysis of DXA FAT% and DXA LEAN% measurements exceed 2.5%. According to commission regulations of the European Community (EEC, 1985), “authorization of the grading methods shall, moreover, be subjected to the root mean square deviation of the errors ($\sqrt{\text{MSE}}$), measured about zero, being less than 2.5” (see also Daumas et al., 1998). Even after a cross-calibration of the DXA scanners involved, all procedures and settings must be identical.

In order to actually verify that the body composition measurements for GE LUNAR DPX (-L, -IQ, -MD) pencil beam DXA scanners are comparable (interchangeable), a study with the same objects scanned on all instruments would be necessary. In animal and veterinary science this objective is still rather difficult to achieve, since the number of DXA scanners in this field of application is restricted to a very few locations around the world and the distances among those few locations are very long.

5. Conclusions

The results of this study indicate that with refinement in procedures, DXA measurements of the live pig can be used to estimate composition of the carcass and *vice versa*. However, measurements need to be standardized with respect to the DXA measurement, the animal and the carcass. For the DXA measurements, the same DXA instrument model, software version, scan mode and method of analysis should be used. To control variation in tissue hydration and fat distribution, the pigs should be of the same genotype, fed similar diets, and scanned at the same stage of maturity. Finally, uniform carcass dissection procedures should be followed.

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